



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Baumgartner, James W.
Farrah, Theresa M.
Foster, Donald C.
Grant, Frank J.
O'Hara, Patrick J.

(ii) TITLE OF INVENTION: Testis-Specific Receptor

(iii) NUMBER OF SEQUENCES: 33

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: ZymoGenetics, Inc.
(B) STREET: 1201 Eastlake Avenue East
(C) CITY: Seattle
(D) STATE: WA
(E) COUNTRY: USA
(F) ZIP: 98102

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Parker, Gary E.
(B) REGISTRATION NUMBER: 31,648
(C) REFERENCE/DOCKET NUMBER: 95-33

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 206-442-6673
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(2) INFORMATION FOR SEQ ID NO:1:

20050727 15:00

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 49..1191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCCCGCCCC GGGAGAGAGG CAATATCAAG GTTTTAAATC TCGGAGAA ATG GCT TTC	57
Met Ala Phe	
1	
GTT TGC TTG GCT ATC GGA TGC TTA TAT ACC TTT CTG ATA AGC ACA ACA	105
Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile Ser Thr Thr	
5 10 15	
TTT GGC TGT ACT TCA TCT TCA GAC ACC GAG ATA AAA GTT AAC CCT CCT	153
Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val Asn Pro Pro	
20 25 30 35	
CAG GAT TTT GAG ATA GTG GAT CCC GGA TAC TTA GGT TAT CTC TAT TTG	201
Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu	
40 45 50	
CAA TGG CAA CCC CCA CTG TCT CTG GAT CAT TTT AAG GAA TGC ACA GTG	249
Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu Cys Thr Val	
55 60 65	
GAA TAT GAA CTA AAA TAC CGA AAC ATT GGT AGT GAA ACA TGG AAG ACC	297
Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr Trp Lys Thr	
70 75 80	
ATC ATT ACT AAG AAT CTA CAT TAC AAA GAT GGG TTT GAT CTT AAC AAG	345
Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys	
85 90 95	

252420: C22GFB80

GGC ATT GAA GCG AAG ATA CAC ACG CTT TTA CCA TGG CAA TGC ACA AAT	393
Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln Cys Thr Asn	
100 105 110 115	
GGA TCA GAA GTT CAA AGT TCC TGG GCA GAA ACT ACT TAT TGG ATA TCA	441
Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr Trp Ile Ser	
120 125 130	
CCA CAA GGA ATT CCA GAA ACT AAA GTT CAG GAT ATG GAT TGC GTA TAT	489
Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp Cys Val Tyr	
135 140 145	
TAC AAT TGG CAA TAT TTA CTC TGT TCT TGG AAA CCT GGC ATA GGT GTA	537
Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly Ile Gly Val	
150 155 160	
CTT CTT GAT ACC AAT TAC AAC TTG TTT TAC TGG TAT GAG GGC TTG GAT	585
Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu Gly Leu Asp	
165 170 175	
CAT GCA TTA CAG TGT GTT GAT TAC ATC AAG GCT GAT GGA CAA AAT ATA	633
His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly Gln Asn Ile	
180 185 190 195	
GGA TGC AGA TTT CCC TAT TTG GAG GCA TCA GAC TAT AAA GAT TTC TAT	681
Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys Asp Phe Tyr	
200 205 210	
ATT TGT GTT AAT GGA TCA TCA GAG AAC AAG CCT ATC AGA TCC AGT TAT	729
Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg Ser Ser Tyr	
215 220 225	
TTC ACT TTT CAG CTT CAA AAT ATA GTT AAA CCT TTG CCG CCA GTC TAT	777
Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Val Tyr	
230 235 240	
CTT ACT TTT ACT CGG GAG AGT TCA TGT GAA ATT AAG CTG AAA TGG AGC	825
Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu Lys Trp Ser	
245 250 255	
ATA CCT TTG GGA CCT ATT CCA GCA AGG TGT TTT GAT TAT GAA ATT GAG	873
Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr Glu Ile Glu	
260 265 270 275	

ATC AGA GAA GAT GAT ACT ACC TTG GTG ACT GCT ACA GTT GAA AAT GAA 921
 Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val Glu Asn Glu
 280 285 290

ACA TAC ACC TTG AAA ACA ACA AAT GAA ACC CGA CAA TTA TGC TTT GTA 969
 Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu Cys Phe Val
 295 300 305

GTA AGA AGC AAA GTG AAT ATT TAT TGC TCA GAT GAC GGA ATT TGG AGT 1017
 Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser
 310 315 320

GAG TGG AGT GAT AAA CAA TGC TGG GAA GGT GAA GAC CTA TCG AAG AAA 1065
 Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu Ser Lys Lys
 325 330 335

ACT TTG CTA CGT TTC TGG CTA CCA TTT GGT TTC ATC TTA ATA TTA GTT 1113
 Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu Ile Leu Val
 340 345 350 355

ATA TTT GTA ACC GGT CTG CTT TTG CGT AAG CCA AAC ACC TAC CCA AAA 1161
 Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr Tyr Pro Lys
 360 365 370

ATG ATT CCA GAA TTT TTC TGT GAT ACA TGAAGACTTT CCATATCAAG 1208
 Met Ile Pro Glu Phe Phe Cys Asp Thr
 375 380

AGACATGGTA TTGACTCAAC AGTTTCCAGT CATGGCCAAA TGTTC AATAT GAGTCTCAAT 1268

AAAC TGAATT TTTCTTGCGA A 1289

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile
 1 5 10 15
 Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val
 20 25 30
 Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
 35 40 45
 Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu
 50 55 60
 Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
 65 70 75 80
 Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
 85 90 95
 Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
 100 105 110
 Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
 115 120 125
 Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
 130 135 140
 Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
 145 150 155 160
 Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
 165 170 175
 Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
 180 185 190
 Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
 195 200 205
 Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
 210 215 220
 Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
 225 230 235 240

000153.0429, 252ED.25T.280

Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu
 245 250 255
 Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr
 260 265 270
 Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val
 275 280 285
 Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu
 290 295 300
 Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
 305 310 315 320
 Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu
 325 330 335
 Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu
 340 345 350
 Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr
 355 360 365
 Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr
 370 375 380

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 10..1152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATCCGCCC	ATG	GCT	TTC	GTT	TGC	TTG	GCT	ATC	GGA	TGC	TTA	TAT	ACC			48
	Met	Ala	Phe	Val	Cys	Leu	Ala	Ile	Gly	Cys	Leu	Tyr	Thr			
	1				5				10							
TTT	CTG	ATA	AGC	ACA	ACA	TTT	GGC	TGT	ACT	TCA	TCT	TCA	GAC	ACC	GAG	96
Phe	Leu	Ile	Ser	Thr	Thr	Phe	Gly	Cys	Thr	Ser	Ser	Ser	Asp	Thr	Glu	
	15					20				25						
ATA	AAA	GTT	AAC	CCT	CCT	CAG	GAT	TTT	GAG	ATA	GTG	GAT	CCC	GGA	TAC	144
Ile	Lys	Val	Asn	Pro	Pro	Gln	Asp	Phe	Glu	Ile	Val	Asp	Pro	Gly	Tyr	
	30				35				40						45	
TTA	GGT	TAT	CTC	TAT	TTG	CAA	TGG	CAA	CCC	CCA	CTG	TCT	CTG	GAT	CAT	192
Leu	Gly	Tyr	Leu	Tyr	Leu	Gln	Trp	Gln	Pro	Pro	Leu	Ser	Leu	Asp	His	
				50					55					60		
TTT	AAG	GAA	TAC	ACA	GTG	GAA	TAT	GAA	CTA	AAA	TAC	CGA	AAC	ATT	GGT	240
Phe	Lys	Glu	Tyr	Thr	Val	Glu	Tyr	Glu	Leu	Lys	Tyr	Arg	Asn	Ile	Gly	
			65				70						75			
AGT	GAA	ACA	TGG	AAG	ACC	ATC	ATT	ACT	AAG	AAT	CTA	CAT	TAC	AAA	GAT	288
Ser	Glu	Thr	Trp	Lys	Thr	Ile	Ile	Thr	Lys	Asn	Leu	His	Tyr	Lys	Asp	
		80					85					90				
GGG	TTT	GAT	CTT	AAC	AAG	GGC	ATT	GAA	GCG	AAG	ATA	CAC	ACG	CTT	TTA	336
Gly	Phe	Asp	Leu	Asn	Lys	Gly	Ile	Glu	Ala	Lys	Ile	His	Thr	Leu	Leu	
	95					100					105					
CCA	TGG	CAA	TGC	ACA	AAT	GGA	TCA	GAA	GTT	CAA	AGT	TCC	TGG	GCA	GAA	384
Pro	Trp	Gln	Cys	Thr	Asn	Gly	Ser	Glu	Val	Gln	Ser	Ser	Trp	Ala	Glu	
	110				115					120					125	
ACT	ACT	TAT	TGG	ATA	TCA	CCA	CAA	GGA	ATT	CCA	GAA	ACT	AAA	GTT	CAG	432
Thr	Thr	Tyr	Trp	Ile	Ser	Pro	Gln	Gly	Ile	Pro	Glu	Thr	Lys	Val	Gln	
				130				135						140		
GAT	ATG	GAT	TGC	GTA	TAT	TAC	AAT	TGG	CAA	TAT	TTA	CTC	TGT	TCT	TGG	480
Asp	Met	Asp	Cys	Val	Tyr	Tyr	Asn	Trp	Gln	Tyr	Leu	Leu	Cys	Ser	Trp	
			145					150					155			
AAA	CCT	GGC	ATA	GGT	GTA	CTT	CTT	GAT	ACC	AAT	TAC	AAC	TTG	TTT	TAC	528
Lys	Pro	Gly	Ile	Gly	Val	Leu	Leu	Asp	Thr	Asn	Tyr	Asn	Leu	Phe	Tyr	
	160						165					170				

TGG	TAT	GAG	GGC	TTG	GAT	CTT	GCA	TTA	CAG	TGT	GTT	GAT	TAC	ATC	AAG	576
Trp	Tyr	Glu	Gly	Leu	Asp	Leu	Ala	Leu	Gln	Cys	Val	Asp	Tyr	Ile	Lys	
175						180					185					
GCT	GAT	GGA	CAA	AAT	ATA	GGA	TGC	AGA	TTT	CCC	TAT	TTG	GAG	GCA	TCA	624
Ala	Asp	Gly	Gln	Asn	Ile	Gly	Cys	Arg	Phe	Pro	Tyr	Leu	Glu	Ala	Ser	
190					195					200					205	
GAC	TAT	AAA	GAT	TTC	TAT	ATT	TGT	GTT	AAT	GGA	TCA	TCA	GAG	AAC	AAG	672
Asp	Tyr	Lys	Asp	Phe	Tyr	Ile	Cys	Val	Asn	Gly	Ser	Ser	Glu	Asn	Lys	
				210					215					220		
CCT	ATC	AGA	TCC	AGT	TAT	TTC	ACT	TTT	CAG	CTT	CAA	AAT	ATA	GTT	AAA	720
Pro	Ile	Arg	Ser	Ser	Tyr	Phe	Thr	Phe	Gln	Leu	Gln	Asn	Ile	Val	Lys	
			225					230					235			
CCT	TTG	CCG	CCA	GTC	TAT	CTT	ACT	TTT	ACT	CGG	GAG	AGT	TCA	TGT	GAA	768
Pro	Leu	Pro	Pro	Val	Tyr	Leu	Thr	Phe	Thr	Arg	Glu	Ser	Ser	Cys	Glu	
		240					245					250				
ATT	AAG	CTG	AAA	TGG	GGC	ATA	CCT	TTG	GGA	CCT	ATT	CCA	GCA	AGG	TGT	816
Ile	Lys	Leu	Lys	Trp	Gly	Ile	Pro	Leu	Gly	Pro	Ile	Pro	Ala	Arg	Cys	
	255					260					265					
TTT	GAT	TAT	GAA	ATT	GAG	ATC	AGA	GAA	GAT	GAT	ACT	ACC	TTG	GTG	ACT	864
Phe	Asp	Tyr	Glu	Ile	Glu	Ile	Arg	Glu	Asp	Asp	Thr	Thr	Leu	Val	Thr	
270					275					280					285	
GCT	ACA	GTT	GAA	AAT	GAA	ACA	TAC	ACC	TTG	AAA	ACA	ACA	AAT	GAA	ACC	912
Ala	Thr	Val	Glu	Asn	Glu	Thr	Tyr	Thr	Leu	Lys	Thr	Thr	Asn	Glu	Thr	
				290						295				300		
CGA	CAA	TTA	TGC	TTT	GTA	GTA	AGA	AGC	AAA	GTG	AAT	ATT	TAT	TGC	TCA	960
Arg	Gln	Leu	Cys	Phe	Val	Val	Arg	Ser	Lys	Val	Asn	Ile	Tyr	Cys	Ser	
			305					310					315			
GAT	GAC	GGA	ATT	TGG	AGT	GAG	TGG	AGT	GAT	AAA	CAA	TGC	TGG	GAA	GGT	1008
Asp	Asp	Gly	Ile	Trp	Ser	Glu	Trp	Ser	Asp	Lys	Gln	Cys	Trp	Glu	Gly	
		320					325					330				
GAA	GAC	CTA	TCG	AAG	AAA	ACT	TTG	CTA	CGT	TTC	TGG	CTA	CCA	TTT	GGT	1056
Glu	Asp	Leu	Ser	Lys	Lys	Thr	Leu	Leu	Arg	Phe	Trp	Leu	Pro	Phe	Gly	
	335					340					345					

00015773 031297

TTC ATC TTA ATA TTA GTT ATA TTT GTA ACC GGT CTG CTT TTG CGT AAG 1104
 Phe Ile Leu Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys
 350 355 360 365

CCA AAC ACC TAC CCA AAA ATG ATT CCA GAA TTT TTC TGT GAT ACA TGAAGACTTT
 1159
 Pro Asn Thr Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr
 370 375 380

CCTCTAGA 1167

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile
 1 5 10 15
 Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val
 20 25 30
 Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
 35 40 45
 Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu
 50 55 60
 Tyr Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
 65 70 75 80
 Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
 85 90 95
 Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
 100 105 110

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Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
115 120 125

Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
130 135 140

Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
145 150 155 160

Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
165 170 175

Gly Leu Asp Leu Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
180 185 190

Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
195 200 205

Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
210 215 220

Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
225 230 235 240

Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu
245 250 255

Lys Trp Gly Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr
260 265 270

Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val
275 280 285

Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu
290 295 300

Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
305 310 315 320

Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu
325 330 335

Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu
340 345 350

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Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr
 355 360 365

Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr
 370 375 380

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Trp Ser Xaa Trp Ser
 1 5

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1126 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 11..1126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACTTGAGAGAA ATG GCT TTC GTC TAC TTG GCT ATC AGA TGC TTA TGT ACC
 Met Ala Phe Val Tyr Leu Ala Ile Arg Cys Leu Cys Thr
 1 5 10

TTT CTG ATA AGC ACA ACA TTC GGC TAT ACT TCA ACT TCA GAC ACC GAG	97
Phe Leu Ile Ser Thr Thr Phe Gly Tyr Thr Ser Thr Ser Asp Thr Glu	
15 20 25	
ATA AAA GTT AAC CCA CCT CAG GAT TTT GAG ATA GTG GAT CCC GGA TAT	145
Ile Lys Val Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr	
30 35 40 45	
TTA GGT TAT CTC TAT TTG CAA TGG CAA CCC CCA CTG TCT CTG GAT AAT	193
Leu Gly Tyr Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp Asn	
50 55 60	
TTT AAG GAA TGC ACA GTG GAA TAT GAA CTA AAA TAC CGA AAC ATT GGT	241
Phe Lys Glu Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly	
65 70 75	
AGT GAA ACA TGG ACG ACC ATC ATT ACT AAG AAT CTA CAT TAC AAA GAT	289
Ser Glu Thr Trp Thr Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp	
80 85 90	
GGG TTT GAT CTT AAC AAG GGC ATT GAA GCG AAG ATA CAC ACA CTT TTA	337
Gly Phe Asp Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu	
95 100 105	
CCA TGG CAA TGC ACA AAT GGA TCA GAA GTT CAA AGT TCC TGG GCA GAA	385
Pro Trp Gln Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu	
110 115 120 125	
GCT ACT TAT TGG ATA TCG CCA CAA GGA ATT CCA GAA ACT AAA GTT CAG	433
Ala Thr Tyr Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln	
130 135 140	
GAT ATG GAT TGT GTA TAT TAC AAT TGG CAA TAT TTA CTC TGT TCT TGG	481
Asp Met Asp Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp	
145 150 155	
AAA CCT GGC ATA GGT GTA CTT CTT GAT ACC AAT TAC AAC TTG TTT TAC	529
Lys Pro Gly Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr	
160 165 170	
TGG TAT GAG GGC TTG GAT CGT GCA TTA CAG TGT GTT GAT TAC ATC AAG	577
Trp Tyr Glu Gly Leu Asp Arg Ala Leu Gln Cys Val Asp Tyr Ile Lys	
175 180 185	

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GTT GAT GGA CAA AAT ATT GGA TGC AGA TTT CCC TAT TTG GAG TCA TCA Val Asp Gly Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ser Ser 190 195 200 205	625
GAC TAT AAA GAT TTC TAC ATT TGT GTT AAT GGA TCA TCA GAA ACC AAG Asp Tyr Lys Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Thr Lys 210 215 220	673
CCT ATC AGA TCC AGT TAT TTC ACT TTT CAG CTT CAA AAT ATA GTT AAA Pro Ile Arg Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys 225 230 235	721
CCT TTG CCA CCA GTC TGT CTT ACT TGT ACT CAG GAG AGT TTA TAT GAA Pro Leu Pro Pro Val Cys Leu Thr Cys Thr Gln Glu Ser Leu Tyr Glu 240 245 250	769
ATT AAG CTG AAA TGG AGC ATA CCT TTG GGA CCT ATT CCA GCA AGG TGT Ile Lys Leu Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys 255 260 265	817
TTT GTT TAT GAA ATT GAG ATC AGA GAA GAT GAT ACT ACC TTG GTG ACT Phe Val Tyr Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr 270 275 280 285	865
ACC ACA GTT GAA AAT GAA ACG TAC ACC TTG AAA ATA ACA AAT GAA ACC Thr Thr Val Glu Asn Glu Thr Tyr Thr Leu Lys Ile Thr Asn Glu Thr 290 295 300	913
CGA CAG TTA TGC TTT GTA GTA AGA AGC AAA GTG AAT ATT TAT TGC TCA Arg Gln Leu Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser 305 310 315	961
GAT GAT GGA ATT TGG AGT GAG TGG AGT GAT AAA CAA TGT TGG GAA GTT Asp Asp Gly Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Val 320 325 330	1009
GAA GAA CTA TTG AAG AAA ACT TTG CTA CTT TTC TTG TTA CCA TTT GGT Glu Glu Leu Leu Lys Lys Thr Leu Leu Leu Phe Leu Leu Pro Phe Gly 335 340 345	1057
TTC ATA TTA ATA TTA GTT ATA TTT GTA ACC GGT CTG CTT TTG TGT AAG Phe Ile Leu Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Cys Lys 350 355 360 365	1105
AGA GAC AGC TAC CCG AAA ATG	1126

00015773.03497

Arg Asp Ser Tyr Pro Lys Met
370

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Phe Val Tyr Leu Ala Ile Arg Cys Leu Cys Thr Phe Leu Ile
1 5 10 15

Ser Thr Thr Phe Gly Tyr Thr Ser Thr Ser Asp Thr Glu Ile Lys Val
20 25 30

Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
35 40 45

Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp Asn Phe Lys Glu
50 55 60

Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
65 70 75 80

Trp Thr Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
85 90 95

Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
100 105 110

Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Ala Thr Tyr
115 120 125

Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
130 135 140

Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
145 150 155 160

000157273280

Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
165 170 175

Gly Leu Asp Arg Ala Leu Gln Cys Val Asp Tyr Ile Lys Val Asp Gly
180 185 190

Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys
195 200 205

Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Thr Lys Pro Ile Arg
210 215 220

Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
225 230 235 240

Pro Val Cys Leu Thr Cys Thr Gln Glu Ser Leu Tyr Glu Ile Lys Leu
245 250 255

Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Val Tyr
260 265 270

Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Thr Thr Val
275 280 285

Glu Asn Glu Thr Tyr Thr Leu Lys Ile Thr Asn Glu Thr Arg Gln Leu
290 295 300

Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
305 310 315 320

Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Val Glu Glu Leu
325 330 335

Leu Lys Lys Thr Leu Leu Leu Phe Leu Leu Pro Phe Gly Phe Ile Leu
340 345 350

Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Cys Lys Arg Asp Ser
355 360 365

Tyr Pro Lys Met
370

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

20250122 15:03:43

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE: .
 (B) CLONE: ZG9801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGGTCCTTCC CATGTTTCAC TACCA

25

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (B) CLONE: ZG9941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTTCGGTATT TTAGTTCATA TTCCA

25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (B) CLONE: ZG9803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

000157-03499

CGGAATTTGG AGTGAGTGGA GTGAT

25

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZG9937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGAAGACCTA TCGAAGAAAA CTTTG

25

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZG9800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGGCTTTTCG TTTGCTTGGC TATCG

25

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZG9802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTCTTGATAT GGAAAGTCTT CATGTATC

28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: AP1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCATCCTAAT ACGACTCACT ATAGGGC

27

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: AP2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACTCACTATA GGGCTCGAGC GGC

23

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ZG9850

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TCTGATAGGC TTGTTCTCTG

20

- (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ZG9851

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATAGCCAAGC AAACGAAAGC

20

- (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ZG9852

00015773 034297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACCTGGCATA GGTGTACTTC

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZG9919

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TTGCCGCCAG TCTATCTTAC

20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZG10317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGGGGGTCTA GAGGAAAGTC TTCATGTATC ACAG

34

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

08015723-031997

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZG10319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGGGGGCTGG AGCTCGGAGA AATGGCTTTC GTT

33

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZG9820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACCCCCACTG TCTCTGGATC ATTTT

25

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZG9806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CACCTTCCCA GCATTGTTTA TCACT

25

(2) INFORMATION FOR SEQ ID NO:24:

262720-041297

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ZG10320

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGGGGGGAGAT CTCAGACAC CGAGATAAAA GTT

33

- (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ZG10318

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGGGGGCTCG AGTTTCTTCG ATAGGTCTTC ACC

33

- (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ZG9882

0901573.031297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTACTCTGTT CTTGGAAACC TGG

23

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZG10082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ACTCTGTTCT TGGAAACCTG G

21

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZG10083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAATGAAACA TACACCTTGA AAAC

24

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

0001573-031297

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZG10081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GCATTGTTTA TCACTCCACT C

21

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZG9881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTCAC TTTGC TTCTTACTAC AAA

23

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZG10389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GACTAGCAGA TCTGGGCTCT TTCTTCGATA GGTCTTCAC

39

20010727 10:44:30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

20